

TOP SECRET

ATATTGGCATGGTGTATGGATGTAATTATTAAGAAAGCAAAAGTCGCTCAATAACT
 TATAACCGTACCACAATACCTACATTAAATAATCTTTCGTTTTCAGCGAGTTATTGA 60

GAGTGGCTTTTTTCTTTGTCTCTCCCTACTGAAAGGAAGTGTCTTACTTGAGTCAA
 CTCACCGAAAAAAGAAACAGGAGAGGGGATGACTTTCCTTCACTAAGAATGAATCAGTT 120

Leu Ser Gln
 Yoml

AACCTCAAAATTATAACCCCGAAGCTGATACCTCATCCAAACTGTGGAACAGTTA
 TTGGAGTTTAAATATGATTGGGGCGTTCGACTATGGAGTAGGTTTGACAGCTTGTCAAT 180

Asn Leu Lys Ile Ile Leu Thr Pro Gln Ala Asp Thr Ser Ser Lys Thr Val Glu Gln Leu
 Yoml

AATCAGCAAATTAAATCCCTGGAAAGAAACTCAACTCCCCTCAAGCTCAATACAAACATT
 TTAGTCGTTTAAATTAGGGACCTTTCCTTTGAGTTGAGGGAGTTCGAGTTATGTTGTAA 240

Asn Gln Gln Ile Lys Ser Leu Glu Lys Lys Leu Asn Ser Leu Lys Leu Asn Thr Asn Ile
 Yoml

FIG. 1A-1

2 / 31

T02F80" 63T2E550

GATTCACAAACCTTAAAGCCTGCAAGAATCTCCCTGCTATCGACACATATCAGAAA
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 CTAAGATGTTGGAATTTTCGAGACGTTCTTAAGAGGAGACGATAGCTGIGTATAGTCTTT 300

Asp Ser Thr Thr Leu Lys Ala Leu Gln Glu Phe Ser Ser Ala Ile Asp Thr Tyr Gln Lys
 -----Yoml-----

AACCTAAAATCCTATATAATCAACAGTTAAAGAAACCTCAACAGTAATTAAGAATGCTGAC
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 TTGGATTTTAGGATATTAGTTTGTCAAATTTCTTTGGAGTGTGTCATTAATTCITACGACTG 360

Asn Leu Lys Ser Tyr Asn Gln Thr Val Lys Glu Thr Ser Thr Val Ile Lys Asn Ala Asp
 -----Yoml-----

GGATCAGTTGAAAAGCTCACCCAGCAGTATAAGAAAAATGGIGAGATACTTCAACGTGAA
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 CCTAGTCAACITTTTCGAGTGGGTGTCATATTCITTTTACCACCTCTAIGAAGTTGCACCT 420

Gly Ser Val Glu Lys Leu Thr Gln Gln Tyr Lys Lys Asn Gly Glu Ile Leu Gln Arg Glu
 -----Yoml-----

ACAAAAATAATCAACAATCGTAATACAGCATTAAAGCAAGAAACTCAAGAGGTTAACAAG
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 TGTTTTATTAGTTGTTAGCATTATGTCGTAATTTCGTTCTTTGAGTTCICCAATTGTTTC 480

Thr Lys Ile Ile Asn Asn Arg Asn Thr Ala Leu Lys Gln Glu Thr Gln Glu Val Asn Lys
 -----Yoml-----

FIG. 1A-2

3 / 31

T04T50" E07E660

CTAACACAGGCCACTGAGAACTAGGACAGGTTCAAAAAAGACTGTGCAGAGAAATCTG
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 GATTGTCCGGTGACTCTTTGATCCCTGTCCTCAAGTTTTTTTTCIGACACGCTCTCTTAGAC
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540

Leu Thr Gln Ala Thr Glu Lys Leu Gly Gln Val Gln Lys Lys Thr Val Gln Arg Asn Leu
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 Yoml

CAAGGACAGCCAACAAGGTAGTGCAGAAAAACCGCCACGGGTTCGATGATATTGTTTAT
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 GTTCCGTCCGGTTGTTCCATCACGCTCTTTTGGCGGTGCCCAAGCTACTATAACAAATA
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600

Gln Gly Gln Pro Thr Lys Lys Val Val Gln Lys Asn Arg His Gly Phe Asp Asp Ile Val Tyr
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 Yoml

ACAACTGATCCTAAAACTAATTCGACCCTCCTCAAAAACTACAACCTAATTATGACCAACAA
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 TGTTGACTAGGATTTTGATTAAAGCTGGAGGAGTTTGTGATGTGATTAAATACGTGTGTT
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660

Thr Thr Asp Pro Lys Thr Asn Ser Thr Ser Ser Lys Thr Thr Thr Asn Tyr Asp Gln Gln
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 Yoml

AGGAGAGCAATTGAGCAGCTTAAGCAAGATTTAGAGAGCTTAGACAGCAAGGTATTGTT
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 TCCTCTCGTTAACTCGTCCGAATTCGTTCTAAATCTCTTCGAATCTGTCGTCCATAACAA
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720

Arg Arg Ala Ile Glu Gln Leu Lys Gln Asp Leu Glu Lys Leu Arg Gln Gln Gly Ile Val
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 Yoml

FIG. 1B-1

4 / 31

ACTGATACGACCAATCTCATCTCTTGGCCGAAAAATAAACACAGCTCAATCCGCTCAACAA 780
 TGACIATGCTGGTAGAGTAGAGAACCGGCTTTTATTGTCGAGTAGCGGAGTTGTT

Thr Asp Thr Thr Ile Ser Ser Leu Gly Arg Lys Ile Asn Thr Ala Gln Ser Ala Gln Gln
 Yomi

ATTGAAGCACTGC AAAATAGGATAAGGATGTTAGATGATAAAATCTGCGGCAGTTGCGAAG 840
 TAACTTCGTGACGTTTTATCCTATTCTCTACAATCTACTATTAGACGCCGTCACGCTTC

Ile Glu Ala Leu Gln Asn Arg Ile Arg Met Leu Asp Asp Lys Ser Ala Ala Val Ala Lys
 Yomi

AACAATGAATTAAAGAAACCAATTGAATTATATCAGCGACAGGCACAAAGTAAATGTTCAA 900
 TTGTTACTTAATTTCCTTTTGGTAACCTTAATATAGTCGCTGCCGTTCAATTACAAGTT

Asn Asn Glu Leu Lys Lys Thr Ile Glu Leu Tyr Gln Arg Gln Ala Gln Val Asn Val Gln
 Yomi

FIG. 1B-2

5 / 31

FO2FB0 0312E650

AACCTAAATACACGGTAIGGCAGTICTATGGGCTCTAGTAATAGACAAGCTGTTCAAGAT
 TTGGATTTATGTGCCATACCGTCAAGATACCCGAGATCATTTATCTGTTCCGACAAGTTCTA 960

Asn Leu Asn Thr Arg Tyr Gly Ser Ser Met Gly Ser Ser Asn Arg Gln Ala Val Gln Asp
 Yoml

TATTTGAATGCAGTAAATAGTCTTAATGTAGCACACGACACGGAAGCAATAATATCAGATCACAA
 ATAAACTTACGTCATTTATCAGAAATTACATTTCGTGACCTTCGTTATTATAGTCTAGTGTT 1020

Tyr Leu Asn Ala Val Asn Ser Leu Asn Val Ser Thr Gly Ser Ser Asn Asn Ile Arg Ser Gln
 Yoml

ATTCAAAGCTTGAATATGCAATTAGAGAATTAGCCTCCAACGCTCAAAACAGCTGCTAAT
 TAAGTTTCGAACCTTATACGTTAAATCTCTTAATCGGAGGTTCGAGTTTGTCGACGATTA 1080

Ile Gln Ser Leu Asn Met Gln Phe Arg Glu Leu Ala Ser Asn Ala Gln Thr Ala Ala Asn
 Yoml

CAAGCCTCTTCTTTTGGAGCAGAACTAACCCAAACCTTCAAAAGCAIGTCCACCTATTTA
 GTTCGGAGAAGAAACCTCGTCTTGATTGGGTTTGAAGTTTTCGTACAGGTGGATAAAT 1140

Gln Ala Ser Ser Phe Gly Ala Glu Leu Thr Gln Thr Phe Lys Ser Met Ser Thr Tyr Leu
 Yoml

FIG. 1C-1

6 / 31

T4T50" 63E660

ATCTCCGGTTCTTTATCTACGGAGCTAICTCTGGACTTAAAGAAATGGTATCCCAGGCA 1200
 TAGAGGCCAAGAAATAAGATGCCTCGATAGAGACCTGAATTTCTTTACCATAGGGTCCGT

Ile Ser Gly Ser Leu Phe Tyr Gly Ala Ile Ser Gly Leu Lys Glu Met Val Ser Gln Ala
 Yoml

ATAGAAATTGATACCTCATGACAAATATTCGCCGIGTTAIGAAIGAGCCGGATTATAAA 1260
 TATCTTTAACTATGAGAGTACTGTTTATAAGCGGCACAACTACTTACICGGCCIAATAITTT

Ile Glu Ile Asp Thr Leu Met Thr Asn Ile Arg Arg Val Met Asn Glu Pro Asp Tyr Lys
 Yoml

TATAATGAACCTTCCCAAGAACTCTATTGACTTAGGTGATACACTTTCAAAATAAAATCACA 1320
 ATATTACTTGAAGAGGTTCTTAGATAAAGTGAATCCACTATGTGAAAAGTTTATTAGTGT

Tyr Asn Glu Leu Leu Gln Glu Ser Ile Asp Leu Gly Asp Thr Leu Ser Asn Lys Ile Thr
 Yoml

GATATTCTTCAAATGACAGGCGATTITGGGAGAAATGGGTTTCGATGAAAGTGAGCTCTCC 1380
 CTATAAGAAGTTTACTGTCCGCTAAACCCCTCTTACCCAAAGCTACTTTCACCTCGAGAGG

Asp Ile Leu Gln Met Thr Gly Asp Phe Gly Arg Met Gly Phe Asp Glu Ser Glu Leu Ser
 Yoml

FIG._1C-2

7 / 31

Y02F30/03669

ACGTTAACGAAACTGCCCAAGTTCTTCAAAAATGTCIGATTAACTCCCGATGATACA
 TGC AATTGCTTTTGACGGGTTCAAGAAGTTTACAGAGACTAAATTGAGGGCTACTATGT
 1440
 Thr Leu Thr Lys Thr Ala Gln Val Leu Gln Asn Val Ser Asp Leu Thr Pro Asp Asp Thr
 Yomi
 GTTAACACTCTAACGGCAGCAATGCTCAACTTTAATAATTGCAGCAAAATGATTCAATATCA
 CAATTGTGAGATTGCCGTCGTTACGAGTTGAATTATAACGTCGTTTACTAAGTTATAGT
 1500
 Val Asn Thr Leu Thr Ala Ala Met Leu Asn Phe Asn Ile Ala Ala Asn Asp Ser Ile Ser
 Yomi
 ATTGCAGATAAAATTAAATGAGGTIGATAATAACTATGCTGTTACAACTCTAGATCTGGCC
 TAACGTCATTTAATTACTCCAACTATTATTGATACGACAAATGTTGAGATCTAGACCGG
 1560
 Ile Ala Asp Lys Leu Asn Glu Val Asp Asn Asn Tyr Ala Val Thr Thr Leu Asp Leu Ala
 Yomi
 AATTCTATCCGTAAAGCTGGTTCAACTGCTTCTACATTCGGGGTAGAGCTAAATGATCTT
 TTAAGATAGGCATTTTCGACCAAGTTGACGAAGATGTAAGCCCCCATCTCGATTACTAGAA
 1620
 Asn Ser Ile Arg Lys Ala Gly Ser Thr Ala Ser Thr Phe Gly Val Glu Leu Asn Asp Leu
 Yomi

FIG. 1D-1

TABLE 1

ATTGGTTATACAACIGCAATTGCTAGTACAAACACGCGTGAATCAGGGAATATCGTCGGGAAC
 TAACCAATAATGTTGACGTTAACGATCAATGTTGTCACCTAGTCCTTATAGCAGCCCTTG
 1680

Ile Gly Tyr Thr Thr Ala Ile Ala Ser Thr Thr Arg Glu Ser Gly Asn Ile Val Gly Asn
 Yomi

TCCTTAAAGACAATTTTCGCGCGGATIGGGAATAATCAAAGCTCAATTAAAGCGTTAGAA
 AGGAATTTCTGTTAAAGCGCGCCTAACCCCTTATTAGTTTCGAGTTAATTCGCAATCTT
 1740

Ser Leu Lys Thr Ile Phe Ala Arg Ile Gly Asn Asn Gln Ser Ser Ile Lys Ala Leu Glu
 Yomi

CAGATIGGTATCTCAGTTAAACACAGCTGGTGGTGAAGCTAAATCAGCAAGTGATTTAATT
 GTCTAACCATAGAGTCAATTTTGTCGACCACCACCTTCGATTAGTCGTTCACTAAATTA
 1800

Gln Ile Gly Ile Ser Val Lys Thr Ala Gly Gly Glu Ala Lys Ser Ala Ser Asp Leu Ile
 Yomi

AGTGAAGTIGCTGGTAAGTGGGATACGCTTCTGATGCTCAGAAACAAATACTTCAATT
 TCACTTCAACGACCATTACCCCTATGCGAAAGACTACGAGTCTTTGTTTGAAGTTAA
 1860

Ser Glu Val Ala Gly Lys Trp Asp Thr Leu Ser Asp Ala Gln Lys Gln Asn Thr Ser Ile
 Yomi

FIG. 1D-2

FIG. 1E-1

GGAGTAGCTGGTATTTATCAATTATCCCGTTTTAATGCAATGATGAACAACTTCTCTATT 1920
 CCTCATCGACCATAAATAGTTAATAGGGCAAAATTACGTTACTTACTTGTGAAGAGATAA
 Gly Val Ala Gly Ile Tyr Gln Leu Ser Arg Phe Asn Ala Met Met Asn Asn Phe Ser Ile
 Yoml
 GCTCAGAATGCGGCTAAAACTGCGGCTAACTCAACAGGAAGTCTTGGAGTGAGCAGCAA 1980
 CGAGTCTTACGCCGATTTTGACGCCGATTGAGTGTGCTTCCACGAACCTCACCTCGTCGTT
 Ala Gln Asn Ala Ala Lys Thr Ala Ala Asn Ser Thr Gly Ser Ala Trp Ser Glu Gln Gln
 Yoml
 AAGTATGCAGATAGTCTACAAGCTAGGGTAAATAAGCTTCAAAATAACTTCACTGAATTT 2040
 TTATACGCTATCAGATGTTTCGATCCCATTTATTCGAAGTTTATTTGAAGTGACTTAAA
 Lys Tyr Ala Asp Ser Leu Gln Ala Arg Val Asn Lys Leu Gln Asn Asn Phe Thr Glu Phe
 Yoml
 GCTATTGCAGCTTCIGATGCTTTTATTAGCGACGGATTAAATGAATTTACTCAAGCCGCA 2100
 CGATAACGTCGAAGACTACGAAAAATAATCGCTGCCTAATTAACTTAAATGAGTTTCGGCGT
 Ala Ile Ala Ala Ser Asp Ala Phe Ile Ser Asp Gly Leu Ile Glu Phe Thr Gln Ala Ala
 Yoml

FIG. 1E-1

10/31

T04T80" ESTE66D

GGTTCCTTGGCTTAACGCTTCTACAGGAGTAATCAAAATCAGTTGGGTTCCTACCTCCCTT
 CCAAGAAACGAATTGCGAAGATGTCCCTCATTAGTTAGTCAACCAAGGATGGAGGGGAA 2160

Gly Ser Leu Leu Asn Ala Ser Thr Gly Val Ile Lys Ser Val Gly Phe Leu Pro Pro Leu
 Yoml

TTAGCTGCAGTAAGCACCTGCAACCCCTTTTGCTCAGTAAGAATACCCGCACATTAGCCAGC
 AATCGACGTCATTTCGTGACGTTGGGAAAACGAGTCATCTTATGGCGTGTAAATCGGTCG 2220

Leu Ala Ala Val Ser Thr Ala Thr Leu Leu Ser Lys Asn Thr Arg Thr Leu Ala Ser
 Yoml

AGCCTAATTTTGGGCACACGTGCAATGGGGCAAGAACTTTAGCGACTGCTGGGCTAGAA
 TCGGATTAAACCCGTTGTCACGTTACCCCGTCTTTGAAATCGCTGACGACCCGATCTT 2280

Ser Leu Ile Leu Gly Thr Arg Ala Met Gly Gln Glu Thr Leu Ala Thr Ala Gly Leu Glu
 Yoml

GCTGGTATGACTCGTGCAGCAGTCGCCCTCAAGAGTTCTAAAACTGCTCTICGAGGGTTG
 CGACCATAGTACTGAGCACGTCGTCAGCGGAGTCTCAAGATTTTGACGAGAAAGCTCCCAAC 2340

Ala Gly Met Thr Arg Ala Ala Val Ala Ser Arg Val Leu Lys Thr Ala Leu Arg Gly Leu
 Yoml

FIG. 1E-2

11 / 31

T04T80" 09T2E660

CTTGTTCAACTTTAGTTGGGGTGCACTTGTCTTGGGATGGGCGCTAGAATCATT
 GAACAAAGTTGAAATCAACCGCCACGTAAACGACGAAACCTACCCGCGATCTTAGTAAT 2400

Leu Val Ser Thr Leu Val Gly Ala Phe Ala Ala Leu Gly Trp Ala Leu Glu Ser Leu
 Yoml

ATTTCTTCTTTTCAGAAAGCTAAAAAGCTAAAGATGATTTTGAGCAGAGCCAGCAAACC
 TAAAGAAGAAACGCTTCGATTTTTCGATTCTACTAAAACTCGTCTCGGTCGTTGG 2460

Ile Ser Ser Phe Ala Glu Ala Lys Lys Ala Lys Asp Asp Phe Glu Gln Ser Gln Thr
 Yoml

AATGTCGAAGCAATTACGACCAATAAAGACTCCACTGATAAACTAATACAGCAATATAAA
 TTACAGCTTCGTTAATGCTGGTTATTCTGAGGTGACTATTGATTATGTCGTTATATT 2520

Asn Val Glu Ala Ile Thr Thr Asn Lys Asp Ser Thr Asp Lys Leu Ile Gln Gln Tyr Lys
 Yoml

GAGCTTCAAAAAGTTAAAGAGTCAAGATCTTTAACTTCAGATGAAGAGCAAGAATACCTT
 CTCGAAGTTTTTCAATTTCTCAGTTCTAGAAAATGAAGTCTACTTCTCGTTCTTATGGAA 2580

Glu Leu Gln Lys Val Lys Glu Ser Arg Ser Leu Thr Ser Asp Glu Glu Gln Tyr Leu
 Yoml

FIG. 1F-1

12 / 31

TATFBD" EST22660

CAAGTCACTCAGCAATTAGCACAAACTTTCCTGCATTAGTTAAAGGCTATGATTCICAA
 GTTCAGTGAGTCGTTAATCGTGTTTGAAAGGGACGTAATCAATTCGATACTAAGAGTT 2640

Gln Val Thr Gln Gln Leu Ala Gln Thr Phe Pro Ala Leu Val Lys Gly Tyr Asp Ser Gln
 _____Yoml_____

GGAAATGCAATTCCTTAAGACAAATAAAGAGCTTGAAAAAGCGATTGAGAATACTAAAGAG
 CCTTACGTTAAGAATTCCTGTTTATTCCTCGAATTTTCGCTAACTCTTATGATTTCTC 2700

Gly Asn Ala Ile Leu Lys Thr Asn Lys Glu Leu Glu Lys Ala Ile Glu Asn Thr Lys Glu
 _____Yoml_____

TATTTGGCTTTAAAGAAACAAGAACAGACAGCGCAAGAAAACATTCGAAGACGCT
 ATAAACCGAAATTCCTTGTTCCTTGTTCCTGTCGCGTTCTTTTGTAAGCTTCTGCGA 2760

Tyr Leu Ala Leu Lys Lys Gln Glu Thr Arg Asp Ser Ala Lys Lys Thr Phe Glu Asp Ala
 _____Yoml_____

TCTAAGGAAATTAAAAAGTCTAAGGATGAATTAAAGCAGTACAAACAATAGCTGACTAC
 AGATTCCTTTAATTTTCAGATTCCTACTTAATTTTCGTCATGTTTGTTCGACTGATG 2820

Ser Lys Glu Ile Lys Lys Ser Lys Asp Glu Leu Lys Gln Tyr Lys Gln Ile Ala Asp Tyr
 _____Yoml_____

FIG._1F-2

13 / 31

AACGATAAAGGTAGACCTAAATGGGATCTCATTCGAGATGACGATGACTATAAGGTTGCA 2880
 TTGCTATTTCCATCTGGATTTACCCCTAGAGTAACGCTCTACTGCTACTGATATTCCAACGT
 Asn Asp Lys Gly Arg Pro Lys Trp Asp Leu Ile Ala Asp Asp Asp Tyr Lys Val Ala
 Yoml
 GCTGATAAAGCTAAACAAAGTATGCTCAAAAGCTCAATCTGACATIGAGAGTGGAAATGCT 2940
 CGACTATTTTCGATTTGTTTCATACGAGTTTCGAGTTAGACGTAACTCTCACCTTTACGA
 Ala Asp Lys Ala Lys Gln Ser Met Leu Lys Lys Ala Gln Ser Asp Ile Glu Ser Gly Asn Ala
 Yoml
 AAAGTTAAAGATAGCGTCTTTCAAATGCAAAATGCTTATAGTTCAATIGATATCAGTAAT 3000
 TTTCAAATTTCTATCGCAGGAAAGTTAACGTTTACGAATATCAAGTTAACTATAGTCATTA
 Lys Val Lys Asp Ser Val Leu Ser Ile Ala Asn Ala Tyr Ser Ser Ile Asp Ile Ser Asn
 Yoml
 ACTTTAAAGACGAGTATTAGTGAATGTTGTCACAACTTAACTTAAAAGATGATTAGAT 3060
 TGAAATTTTCGCTCATAATCACTACAACAGTTGTTGAATGAATTTTCTACTAAATCTA
 Thr Leu Lys Thr Ser Ile Ser Asp Val Val Asn Lys Leu Asn Leu Lys Asp Asp Leu Asp
 Yoml

FIG. 1G-1

14 / 31

T04T80" 68T26660

CCTGAAGAATTAGAAAAATCTCCTCTCTTTAGGAAAGCTTCAAGAAAAATGCAAAAA
 GGACTTCTTAATCTTTTAAGAGGAGAGAAATCCTTTCGAAGTCTTTTTTACGTTTTT 3120

Pro Glu Leu Glu Lys Phe Ser Ser Ser Leu Gly Lys Leu Gln Glu Lys Met Gln Lys
 — Yoml —

GCTTTAGATTGAGGCGATGAAAAAGCTTTCGATAACGCAAAAAAGATCTTCAAAGTCTC
 CGAAATCTAAGTCCGCTACTTTTTCGAAAGCTATTCGGTTTTTCTAGAAAGTTTCAGAG 3180

Ala Leu Asp Ser Gly Asp Glu Lys Ala Phe Asp Asn Ala Lys Lys Asp Leu Gln Ser Leu
 — Yoml —

TTGGAACATACITCCAAATCCGATTCCTCTCTATGATGTTTTTAAATGAGCTTCGACAAA
 AACCTTTGTATGAGGTTTAGGCTAAGAAGATACTACAAAAATTTTACTCGAAGCTGTTT 3240

Leu Glu Thr Tyr Ser Lys Ser Asp Ser Ser Ile Asp Val Phe Lys Met Ser Phe Asp Lys
 — Yoml —

GCACAGAAGAACATAAAGATGGAGATAAGAGCTTATCTTCGTCAAATCIGAAGTTGGT
 CGTGCTCTCTTGATTTTCTACCTCTATCTCGAATAGAGGCAGTTTAGACTTCAACCA 3300

Ala Gln Lys Asn Ile Lys Asp Gly Asp Lys Ser Leu Ser Ser Val Lys Ser Glu Val Gly
 — Yoml —

FIG._1G-2

15 / 31

T02F80" E8T2E660

GATTTAGGTGAGACGCTGGCAGAGCAGGTAACGAGGCAGAGATTTGGTAAGAAGCTA 3360
 CTAATCCACTCTGCAGCCGCTCTCGTCCATTGCTCCGCTCTCTAAACCAATCTTCGAT

Asp Leu Gly Glu Thr Leu Ala Glu Ala Gly Asn Glu Ala Glu Asp Phe Gly Lys Lys Leu
 Yoml

AAAGAAAGCTCTGGATGCAAAATAGTGTGATGATATTAAGGCAGCTATTAAAGAAATGTCA 3420
 TTCTTCGAGACCTACGTTTATCACAACACTACTATAATCCGTCGATAATTCTTTACAGT

Lys Glu Ala Leu Asp Ala Asn Ser Val Asp Asp Ile Lys Lys Ala Ala Ile Lys Glu Met Ser
 Yoml

GATGCTATGCAGTTCGATTCCGTTCAAGATGCTTAAATGGGGAATTTTTAAATACACC 3480
 CTACGATACGTCAGCTAAGGCAAGTTCACAGAAATTACCCCTATAAAAATTATTGTGG

Asp Ala Met Gln Phe Asp Ser Val Gln Asp Val Leu Asn Gly Asp Ile Phe Asn Asn Thr
 Yoml

AAAGATCAAGTAGCTCCTCTCAATGATCTTCTGGAAAAAATGGCTGAAGGTAAAAGTATT 3540
 TTTCTAGTTCATCGAGGAGAGTTACTAGAAGACCTTTTTTACCGACTTCCATTTTCATAA

Lys Asp Gln Val Ala Pro Leu Asn Asp Leu Leu Glu Lys Met Ala Glu Gly Lys Ser Ile
 Yoml

FIG. 1H-1

16 / 31

TOTAL "EST" 660

TCTGCAAAATGAAGCTAATACCCCTTATTCAAAAAGATAAGGAACTTGCCAGGCTATTAGC
 AGACGTTTACTTCGATTATGGGAATAAGTTTCTATCTTGAACGGGICCGATAATCG
 3600

Ser Ala Asn Glu Ala Asn Thr Leu Ile Gln Lys Asp Lys Glu Leu Ala Gln Ala Ile Ser
 Yoml

ATCGAAAAATGGCGTTGIGAAAAATTAAACCGTGATGAAGTTATCAACAAGAAAAAGTTAAA
 TAGCTTTTACCGCAACACTTTTAATTGGCACTACTTCAATAGTTTCTTTTCAATTT
 3660

Ile Glu Asn Gly Val Val Lys Ile Asn Arg Asp Glu Val Ile Lys Gln Arg Lys Val Lys
 Yoml

CTIGATGCTTATAACGACATGGTTACCTACAGCAATAAATTGATGAAAACAGAAGTTAAC
 GAACTACGAATATTGCTGTACCAATGGATGTCGTTATTAACTACTTTTGTCTTCAATTG
 3720

Leu Asp Ala Tyr Asn Asp Met Val Thr Tyr Ser Asn Lys Leu Met Lys Thr Glu Val Asn
 Yoml

AACGCTATCAAAACTTTAAACGCTGATACCTTACGGATTGACAGCCTGAAAAAGCTACGA
 TTGCGATAGTTTIGAAATTTGCGACTATGGAATGCCTAACTGTCGGACTTTTTCGATGCT
 3780

Asn Ala Ile Lys Thr Leu Asn Ala Asp Thr Leu Arg Ile Asp Ser Leu Lys Lys Leu Arg
 Yoml

FIG. 1H-2

17 / 31

"04T30" 68T22660

AAAGAACGAAAGCTTGATAIGTCTGAGGCCGAACCTGTCAGACCTAGAAGTTAAGTCAATT
 +-----+-----+-----+-----+-----+-----+-----+-----+
 TTTCITGCTTTCGAACTATACAGACTCCGGCTTGACAGCTCGGATCTTCAATTCAGTTAA
 3840

Lys Glu Arg Lys Leu Asp Met Ser Glu Ala Glu Leu Ser Asp Leu Glu Val Lys Ser Ile
 -----Yoml-----

AATAATGTTGCAGATGCAAAAAAGAACTTAAAAAGCTTGAGAGAGAAAAATGCTTCAACCT
 +-----+-----+-----+-----+-----+-----+-----+-----+
 TTATTACAACGCTACGTTTTTTTCTTGAATTTTTCGAACTTCCTCTTTTACGAAAGTTGGA
 3900

Asn Asn Val Ala Asp Ala Lys Lys Glu Leu Lys Lys Leu Glu Glu Lys Met Leu Gln Pro
 -----Yoml-----

GGTGGATACTCCAATAGTCAAAATGAAGCAATGCAAAGCGTTAAATCAGCTTTAGAATCT
 +-----+-----+-----+-----+-----+-----+-----+-----+
 CCACCTATGAGGTTATCAGTTTAACTTCGTTACGTTTCGCAATTTAGTCGAAATCTTAGA
 3960

Gly Gly Tyr Ser Asn Ser Gln Ile Glu Ala Met Gln Ser Val Lys Ser Ala Leu Glu Ser
 -----Yoml-----

TATATTTCTGCAATCIGAAGAAGCCACCAGTACACAGAATAATGAATAAACAGGCACCTTGTT
 +-----+-----+-----+-----+-----+-----+-----+-----+
 ATATAAGACGTAGACTTCTTCGGTGGTCAIGTGTCTTACTTATTGTCCGCGAACA
 4020

Tyr Ile Ser Ala Ser Glu Glu Ala Thr Ser Thr Gln Glu Met Asn Lys Gln Ala Leu Val
 -----Yoml-----

FIG. 11-1

GAAGCTGGAACATCATTGGAGAAATGGACAGATCAACAAGAAAAGCCAATGAAGAAACC
 CTTCGACCTTGTAGTAACCCTTAACCTGCTAGTGTCTTTTCGGTTACTTCTTTGG
 4080

Glu Ala Gly Thr Ser Leu Glu Asn Trp Thr Asp Gln Gln Glu Lys Ala Asn Glu Glu Thr
 Yomi

AAGACTTCCAIGTATGTTGTGATATAATACAAGGAAGCATTAGAAAAAGTTAATGCTGAG
 TTCTGAAGGTACATACAACAACIATTTAATGTTCTTCGTAATCTTTTCAATTACGACTC
 4140

Lys Thr Ser Met Tyr Val Val Asp Lys Tyr Lys Glu Ala Leu Glu Lys Val Asn Ala Glu
 Yomi

ATTGACAAGTACAACAAGCAGGTCATGATTATCTTAATACTCTCAGAAATATCGAGAT
 TAACTGTTCAATGTTGTTTCGTCAGTTACTAATAGGATTTATGAGAGTCTTTATAGCTCTA
 4200

Ile Asp Lys Tyr Asn Lys Gln Val Asn Asp Tyr Pro Lys Tyr Ser Gln Lys Tyr Arg Asp
 Yomi

GCAATCAAGAAAGAAATTAAAGCACTTCAGCAAAAAGAAAGCTTATGCAGGAACAAGCT
 CGTTAGTTCITTTTAAATTCGTAAGTCGTTTCTTTTCGAATACGTCCTTGTTCGA
 4260

Ala Ile Lys Lys Glu Ile Lys Ala Leu Gln Gln Lys Lys Lys Leu Met Gln Glu Gln Ala
 Yomi

FIG. 11-2

19 / 31

4320
 4380
 4440
 4500

AAGCTGCTTAAAGATCAAAATTAAATCCGGTAACATTACTCAATACGGTATTGTAACCTCT
 TTCGACGAATTTCTAGTTAAATTTAGGCCATTGTAAATGAGTTATGCCATAACATTGGAGA

Lys Leu Leu Lys Asp Gln Ile Lys Ser Gly Asn Ile Thr Gln Tyr Gly Ile Val Thr Ser
 Yomi

ACAACTTCTTCIGGTGGAACCCCTCTCAACTGGTGGATCATATTCAGGCAAGTATTCA
 TGTGAAGAAGACCACCTTGGGGGAGGAGTTGACCACCTAGTATAAGTCCGTTTCATAAGT

Thr Thr Ser Ser Gly Gly Thr Pro Ser Ser Thr Gly Gly Ser Tyr Ser Gly Lys Tyr Ser
 Yomi

AGCTACATAAAATTCAGCAGCTAGTAAATACAAATGTTGACCCCTTGCCCTTATTGCAGCTGTA
 TCGATGTATTTAAGTCGTCGATCATTTATGTTACAACCTGGGACGGGAATAACGTCGACAT

Ser Tyr Ile Asn Ser Ala Ala Ser Lys Tyr Asn Val Asp Pro Ala Leu Ile Ala Ala Val
 Yomi

ATTCAGCAAGAATCAGGGTTTAAATGCTAAAGCACGATCTGGTGTAGGTGCCATGGGATTA
 TAAGTCGTTCTTAGTCCCAAAATTACGATTTTCGTGTAGACCACATCCACGGTACCCCTAAT

Ile Gln Gln Glu Ser Gly Phe Asn Ala Lys Ala Arg Ser Gly Val Gly Ala Met Gly Leu
 Yomi

FIG._1J-1

20 / 31

SEQ ID NO: 1

ATGCAACTGATGCCAGCAACAGCAAAAAGCTTAGGAGTAAATAACGCTTACGATCCTTAT
 TACGTTGACTACGGTCGTTGTCGTTTTTCGAATCCTCATTIATTGCGAATGCTAGGAATA
 4560

Met Gln Leu Met Pro Ala Thr Ala Lys Ser Leu Gly Val Asn Asn Ala Tyr Asp Pro Tyr
 Yomi

CAAAATGTTATGGGTGGAACAAAGTACCICGCCCCAACAACTTGAAAAGTTTGGCGGTAAT
 GTTTACAATACCCACCCTTGTTTCATGGAGCGGGTTGTTGAACTTTTCAAAACCGCCCATTA
 4620

Gln Asn Val Met Gly Gly Thr Lys Tyr Leu Ala Gln Gln Leu Glu Lys Phe Gly Gly Asn
 Yomi

GTTGAAAAGCATTTGGCTGCATATAATGCTGGGCCTGGTAAACGTAATAATAATGTTGGT
 CAACTTTTTCGTAAACCGACGTATATTACGACCCGGACCATTCGCAATTAATTATACCACCA
 4680

Val Glu Lys Ala Leu Ala Ala Tyr Asn Ala Gly Pro Gly Asn Val Ile Lys Tyr Gly Gly
 Yomi

ATCCCTCCTTTTAAAGAAACACAGAATTACGTCAAGAAGATCATGGCCAACTATAGCAAA
 TAGGGAGGAAAAATTTCTTTGTGICITTAATGCAGTTCTTCTAGTACCGTTGATATCGTTT
 4740

Ile Pro Pro Phe Lys Glu Thr Gln Asn Tyr Val Lys Lys Ile Met Ala Asn Tyr Ser Lys
 Yomi

FIG. 1J-2

21 / 31

T04T80" E8T2E660

TCGCTCATCIGCCACTTCTTCAATCGCCAGCTATTATACAAATAATAGCGCTTTTAGG
 AGCGAGAGTAGACGGTGAAGAAGTTAGCGGTCGATAATAATGTTTATTATCGCGAAAAATCC 4800

Ser Leu Ser Ser Ala Thr Ser Ser Ile Ala Ser Tyr Tyr Thr Asn Ser Ala Phe Arg
 Yoml

GTAAGCTCCAAATAIGGACAACAGGAATCTGGTCTCCGCTCCTCCCCACACAAAGGAACT
 CATTGAGGTTTATACCTGTTGCTTAGACCAGAGCGGAGGGGTGTTTTCCTTGA 4860

Val Ser Ser Lys Tyr Gly Gln Gln Glu Ser Gly Leu Arg Ser Ser Pro His Lys Gly Thr
 Yoml

GATTTTGCTGCAAAAGCAGGTACAGCAATTAAATCTCTTCAAAAGTGGTAAAGTCCAAAT
 CTAAACGACGTTTTCGTCCATGTCGTTAATTAGAGAAGTTTACCATTTCAGGTTTAA 4920

Asp Phe Ala Ala Lys Ala Gly Thr Ala Ile Lys Ser Leu Gln Ser Gly Lys Val Gln Ile
 Yoml

GCTGGCTACAGTAAACTGCAGGTAACTGGGTGTTATTAAACAGGATGATGGAACAGTT
 CGACCGATGTCATTTTGACGTCCATTGACCCCAACAATAATTGTCCTACTACCTTGTCAC 4980

Ala Gly Tyr Ser Lys Thr Ala Gly Asn Trp Val Val Ile Lys Gln Asp Asp Gly Thr Val
 Yoml

FIG. 1K-1

22 / 31

TCTT30" 43T22660

GCCAAGTACATGCCTTAACACTCCTTCTGTAAAGCAGGTCATCAGTTAAAGCC
 CCGTTTCATGTACGTGTACGAATTGTGAGGAAGACATTTTCGTCAGTTAGTCAATTTCGG 5040

Ala Lys Tyr Met His Met Leu Asn Thr Pro Ser Val Lys Ala Gly Gln Ser Val Lys Ala
 Yoml

GGTCAAACTATTGGTAAAGTTGGTAGTACAGGGAACTCGACTGGGAACCACCTTCATTTA
 CCAGTTTGATAACCAATTTCAACCATCATGTCCCTTGAGCTGACCCCTTGGTGAAGTAAAT 5100

Gly Gln Thr Ile Gly Lys Val Gly Ser Thr Gly Asn Ser Thr Gly Asn His Leu His Leu
 Yoml

CAGATCGAACAAAAATGGAAAAACAATCGATCCTGAAAAGTACATGCAAGGTATTGGAAC
 GTCTAGCTTGTTTACCTTTTGTAGCTAGGACTTTTCAATGTACGTTCCATAACCTTGA 5160

Gln Ile Glu Gln Asn Gly Lys Thr Ile Asp Pro Glu Lys Tyr Met Gln Gly Ile Gly Thr
 Yoml

TCTATTTTCAGATGCGTACACAAGCTGAGGCAGAACGACAACAAGGATAGCTCAGGCTAAA
 AGATAAAGTCTACGCAGTGTTCGACTCCGTCITGCTGTGTTCCCTATCGAGTCCGATTT 5220

Ser Ile Ser Asp Ala Ser Gln Ala Glu Ala Glu Arg Gln Gln Gly Ile Ala Gln Ala Lys
 Yoml

FIG. 1K-2

FIG. 1L-1

TCIGATCTTCTCTCCCTCCAAGGAGATATCAGTTCAGTCAATGATCAGATCAAGAAGCTT
 AGACTAGAAGAGAGGGAGGTTCTCTATAGTCAAGTCAGTTACTAGTCTAAGTTCTTGAA
 5280

Ser Asp Leu Leu Ser Leu Gln Gly Asp Ile Ser Ser Val Asn Asp Gln Ile Gln Glu Leu
 Yoml

CAGTATGAACCTAGTTCAATCTAAACTCGATGAGTTTGATAAAAGAAATGGAGATTTTGAT
 GTCATACCTTGATCAAGTTAGATTGAGCTACTCAAACCTAATTTCTTAACCTCTAAACCTA
 5340

Gln Tyr Glu Leu Val Gln Ser Lys Leu Asp Glu Phe Asp Lys Arg Ile Gly Asp Phe Asp
 Yoml

GTTCGGATAGCAAAAGATGAGTCAATGGCTAACAGATACACTTCTGACAGCAAGGAATTC
 CAAGCCTATCGTTTCTACTACAGTTACCGATTGCTATGTGAAGACGTGCTCCTTAAG
 5400

Val Arg Ile Ala Lys Asp Glu Ser Met Ala Asn Arg Tyr Thr Ser Asp Ser Lys Glu Phe
 Yoml

CGAAAAATACACCTCTGATCAGAAAAAAGCTGTGGCAGAGCAAGCTAAAAATCCAACAACAA
 GCTTTTATGTGGAGACTAGTCTTTTTTCGACACCGCTCCTCGATTTCGATTTCGTTGTTGTT
 5460

Arg Lys Tyr Thr Ser Asp Gln Lys Lys Ala Val Ala Glu Gln Ala Lys Ile Gln Gln Gln
 Yoml

FIG. 1L-1

24 / 31

TABLE 1

AAAGTTAATTGGATTCAAAAAGAAATTAAACAAATAAAGCATTGAACTCCGCTCAACGT
 TTTCAATTAAACCTAAGTTTTCTTTAATTGTTTATTTCGTAACCTGAGGCGAGTTGCA 5520

Lys Val Asn Trp Ile Gln Lys Glu Ile Lys Thr Asn Lys Ala Leu Asn Ser Ala Gln Arg
 Yoml

GCACAGCTTCAAGAAGAGCTTAAACAGGCCAAGCTAGATTTAATTTCTGTTCAGACCAG
 CGGTGCGAAGTTCTTCTCGAATTGTCCGGTTCGATCTAAATTAAAGACAAGTTCTGGTC 5580

Ala Gln Leu Gln Glu Leu Lys Gln Ala Lys Leu Asp Leu Ile Ser Val Gln Asp Gln
 Yoml

GTTGCGTGAGCTACAGAAACAACCTTGTTCAATCTAAAGTIGATGAGACACTTAAGTCAATT
 CAAGCACTCGATGCTCTTGTGTAACAAGTTAGATTTCAACTACTCTGTGAATTCAGTTAA 5640

Val Arg Glu Leu Gln Lys Gln Leu Val Gln Ser Lys Val Asp Glu Thr Leu Lys Ser Ile
 Yoml

GAAAAGTCATCTTCTAAAACCCCAAGGAAAAATTAAAGATGTCGATAACAAAATTTCAATG
 CTTTTCAGTAGAAGATTTGGGTTCCCTTTTAAATTTCTACAGCTATTGTTTTAAAGTTAC 5700

Glu Lys Ser Ser Ser Lys Thr Gln Gly Lys Ile Lys Asp Val Asp Asn Lys Ile Ser Met
 Yoml

FIG. 1L-2

25 / 31

TATB0" 63T2660

ACTGAAGAAGATGAAGACAAGGTAAATACTATAGCAAGCAAATAAAGCTCATTCAACAA
 TGACTTCTTCTACTTCTGTTCCAAATTATGATATCGTTCGTTTATTCGAGTAAAGTTGTT
 5760

Thr Glu Glu Asp Glu Asp Lys Val Lys Tyr Tyr Ser Lys Gln Ile Lys Leu Ile Gln Gln
 Yoml

CAACAAAAGGAAGCGAAGAAATACATTAAAGCAGCTTGAAGAACAAAGAAAGCTGCGAAA
 GTTGTTCCTTCGCTTCTTTAIGTAAATTCGTCGAACCTTCTTGTTCGACGCTTT
 5820

Gln Gln Lys Glu Ala Lys Lys Tyr Ile Lys Gln Leu Glu Gln Lys Lys Ala Ala Lys
 Yoml

GGTTTCCCTGACATCCAGGAACAGATCACTGAAGAAATGCAAACTGGAAAGATAAACAG
 CCAAGGGACTGTAGGTCTTGTCTAGTGACTTCTTACGTTTGACCTTCTATTGTC
 5880

Gly Phe Pro Asp Ile Gln Glu Gln Ile Thr Glu Glu Met Gln Asn Trp Lys Asp Lys Gln
 Yoml

AAAGATTTTAACCTTGAGCTTTTATAACACCAAGAAGTCGATCAAGGATATCTATAAATCA
 TTTCTAAAATTGGAACTCGAAATATTGTGGTTCTTCAGCTAGTTCCTATAGATATTAGT
 5940

Lys Asp Phe Asn Leu Glu Leu Tyr Asn Thr Lys Lys Ser Ile Lys Asp Ile Tyr Lys Ser
 Yoml

FIG. 1M-1

26 / 31

T04T80" 6922660

TTGGCTGATGAAGTTGTATCCATCTACAAAGAGATGTACGAAAAAATGCGTGATATTGAG 6000
 AACCGACTACTTCAACATAGGTAGATGTTCTCTACATGCTTTTTTACGCACTATAACTC

Leu Ala Asp Glu Val Val Ser Ile Tyr Lys Glu Met Tyr Glu Lys Met Arg Asp Ile Glu
 Yoml

TTAGAAGCGCATCAGAAAGCGACTCAAGACTTIGATCGATGAGATAGACAAGACTGATGAC 6060
 AATCTTCGCGTAGTCITTCGCTGAGTCTTGAAGTCTACTCTATCTGTCTGACTACTG

Leu Glu Ala His Gln Lys Ala Thr Gln Asp Leu Ile Asp Glu Ile Asp Lys Thr Asp Asp
 Yoml

GAGGCTAAATTTCAAAGAATTAAAGAAAGACAAGACAGTATTCAAAAGTTGACTGAC 6120
 CTCGGATTTAAAGTTTTCTTAATTTCTTCTGTTCTGTCATAGTTTCAACTGACTG

Glu Ala Lys Phe Gln Lys Glu Leu Lys Glu Arg Gln Asp Ser Ile Gln Lys Leu Thr Asp
 Yoml

CAAATTAATCAATACTCCTTGAIGATTTCGAATTCGAAAGTCAAAAGTCAAAGAAGTAA 6180
 GTTAAATTAGTTATGAGAGAAGTAAAGACTTAAGCCCTTCAGTTTTCAGTTTCTTGAT

Gln Ile Asn Gln Tyr Ser Leu Asp Asp Ser Glu Phe Gly Lys Ser Lys Val Lys Glu Leu
 Yoml

FIG. 1M-2

27 / 31

600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

ACTGAACAGCTTCAAAAAGAGCAGTTAGACCTTGATGATTTTCTAAAGGATCGCGAAAGT
 TGACTTGTGCGAAGTTTTCTCGTCAATCTGGAACCTACTAAAAGATTTCCTAGCGCTTICA 6240

Thr Glu Gln Leu Gln Lys Glu Gln Leu Asp Leu Asp Phe Leu Lys Asp Arg Glu Ser
 Yoml

AACAAACGGAAAGAGCGCTCCAAGATCAGCTCGAAAAAGATGAGGAGTCAATCAACAAT
 TTGTTTGCCTTTCTTCGCGAGGTCTAGTCGAGCTTTTCTACTCCTCAGTTAGTTGTTA 6300

Asn Lys Arg Lys Glu Ala Leu Gln Asp Gln Leu Glu Lys Asp Glu Ser Ile Asn Asn
 Yoml

AAATACGATAATCTTGTAATGATGAACGAGCCTTTAAAAAGCTTGAGGATAAGATTATG
 TTTATGCTATTAGAACATTTACTACTTGCTCGGAAATTTTCGAACTCCTATCTAATAC 6360

Lys Tyr Asp Asn Leu Val Asn Asp Glu Arg Ala Phe Lys Lys Leu Glu Asp Lys Ile Met
 Yoml

AATGGAAAAATCACCAGATATCGCTAAGCAGCTTAATGAGTTTCTAAGTTTATTAATACC
 TTACCTTTTATAGTGGCTATAGCGATTGCTCGAATTACTCAAAAGATTCAAAATAATTATGG 6420

Asn Gly Lys Ile Thr Asp Ile Ala Lys Gln Leu Asn Glu Phe Ser Lys Phe Ile Asn Thr
 Yoml

FIG. 1N-1

28 / 31

T04T00" 03T2000

AATATGGAGTCCATTGGAAAAAGTATTTCAAAACAACCTGATGATAAACTCAAAGAAGCA
 TTAACCTCAGGTAACCTTTTTCATAAAGTTTGTGGACTAACTATTGAGTTTCTTCGT
 6480

Asn Met Glu Ser Ile Gly Lys Ser Ile Ser Asn Asn Leu Ile Asp Lys Lys Lys Glu Ala
 Yoml

TCTAATGCACCTGAATACTGCTGTCAAAGGCAACACGACAGGTAAAAAAGTATCCCTTTTC
 AGATTACGTGACTTAIGACGACAGTTTCCGTTGTGCTGTCCATTTTTCATAGGAGAAAG
 6540

Ser Asn Ala Leu Asn Thr Ala Val Lys Gly Asn Thr Thr Gly Lys Lys Val Ser Ser Phe
 Yoml

GCTTCTGGAGGGTACACTGGAAACAGGATTAGGTGCTGGTAAACTTGCAATTCCTACATGAC
 CGAAGACCTCCCAITGACCTTGTCCTAATCCACGACCATTTGAACGTAAGGATGTACTG
 6600

Ala Ser Gly Gly Tyr Thr Gly Thr Gly Leu Gly Ala Gly Lys Leu Ala Phe Leu His Asp
 Yoml

AAAGAACTGATCTTAAATAAAACTGACACAGCCCAACATCCTTGATACGGTAAAAGCTGTT
 TTTCTTGACTAGAAATTTATTGTGACTGTGTCGGTTGTAGGAACATGCCATTTTCGACAA
 6660

Lys Glu Leu Ile Leu Asn Lys Thr Asp Thr Ala Asn Ile Leu Asp Thr Val Lys Ala Val
 Yoml

FIG. 1N-2

29 / 31

T4T3D* 63T2E6G

CGTGAAACCGCTGTGGACGATTCCCAAAATGGGGCCAAGGAGTAAAATTAGCAGACCTT
 +-----+-----+-----+-----+-----+-----+-----+-----+
 GCACCTTGGCGACACCTGCTAAGGGGTTTTACCCCGGTTCCCTCATTTTAAATCGTCGGAA
 6720

Arg Glu Thr Ala Val Asp Asp Ser Pro Lys Trp Gly Gln Gly Val Lys Leu Ala Asp Leu
 -----Yoml-----

ATTAAAAAGGAATTACTTCTATTCCTTCATTAGTTCTCTAACGTTAATCAATCAATGTTA
 +-----+-----+-----+-----+-----+-----+-----+-----+
 TAAATTTTTCCTTAATGAAGATAAGGAAGTAATCAAGGATTGCAATTAGTTAGTTACAAT
 6780

Ile Lys Lys Gly Ile Thr Ser Ile Pro Ser Ser Leu Val Pro Asn Val Asn Gln Ser Met Leu
 -----Yoml-----

ACAAACAGTTTAAATTCCAAATTTAAAGAAGATTGAGATCCCCCTCAAAAACAATTGCTTCT
 +-----+-----+-----+-----+-----+-----+-----+-----+
 TGTITGTCAAATTAAGGTTTAAATTTCTTAACTCTAGGGGAGTTTIGTTAACGAAGA
 6840

Thr Asn Ser Leu Ile Pro Asn Leu Lys Lys Ile Glu Ile Pro Ser Lys Thr Ile Ala Ser
 -----Yoml-----

TCTGGAGATAAAACAATTAAATTTAACGAATACTTTCCACATTGATAAGCTAATAGGAGGA
 +-----+-----+-----+-----+-----+-----+-----+-----+
 AGACCTCTATTTGTAAATTAATTAATTTGCTTAAGAAAGGTGTAACATAATTCGATTATCCTCCT
 6900

Ser Gly Asp Lys Thr Ile Asn Leu Thr Asn Thr Phe His Ile Asp Lys Leu Ile Gly Gly
 -----Yoml-----

FIG. 10-1

30 / 31

T32130" 6372659

GAATCGGGAGCGAGATCGATGTTGAAAGCATTAAAAACGAAAGTGTAAAACTAAATGGT
 CTTAGCCCTCGCTCTAGCTACAAACTTTCGTAATTTTGCTTCAACATTTTGATTACCA 6960

Glu Ser Gly Ala Arg Ser Met Phe Glu Ser Ile Lys Asn Glu Val Lys Leu Asn Gly
 — Yoml —

AGCATGTAAGAGTCTGCAAAAGCAGACICTTTATTTAACTTAACTTGAGGTGGAAACTCA
 TCGTACATTTCTCAGACGTTTTTCGCTCGAGAAATAAATTGAATTGAACCTCCACCTTTGAGT 7020

Ser Met
 — Yoml —

TGATTAGAGAAAGTCAATACTTTATGTTCAATAATATCCCTTCTTAATGAATTAGGAGCCG
 ACTAATCTCTTTCAGTTATGAAATACAAGTTATTATAGGGAAGAATACTTAATCCTCGGC 7080

TAAATGTAAATACAGAAGGA
 ATTIACATTATGCTCTCCT 7100

FIG. 10-2

31 / 31

FIG. 2

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lasa_psea.pe 60 70 80 90 100 110
PKVLLTLMVMQSGPLGAPDERALAAPLGRLSAKRGFD-AQVRDVLQQLSRRYYGFEYQL
YOMI IVTSTTSSGGTPSSTGGSYSGYSSYINSAASKYNVDPALIAAVIQQES-----GFN----
1400 1410 1420 1430 1440 1450

lasa_psea.pe 120 130 140 150 160 170
RQAAARKAVGEDGLNA---ASAALLGLLREGAKVSAVQGNPLGAYAQTFQRLFGTPAAE
YOMI I:::II II I:I II: :I::: II::: II:::
--AKARSGVGAMGLMQLMPATAKSLGVNNAYDPYQNVMMGGTKY--LAQQLEK-FGGNVEK
1460 1470 1480 1490 1500

lasa_psea.pe 180 190 200 210 220
LLQPSNRVARQLQAKAALAPPSNLMQLPWRQ---GYSWQPNGAHSNTGSGYPYSS-FDAS
YOMI I::: II::: I::: I::: I::: I::: I::: I::: I::: I:::
ALAAYNAGPGNV-IKYGIPPFKETQNYVKKIMANYSKSLSSATSSIASYYTNNSAFRVS
1510 1520 1530 1540 1550 1560

lasa_psea.pe 230 23 240 250 260 270
YDWPWGSATYSV-----VAAHAGT-VRVLSRCQVRVTHPSGWATNYY--HMDQIQVSN
YOMI : : I: I::: I: I::: I: I::: I: I::: I: I:::
SKYQQESGLRRSPHKGTDFAAKAGTAIKSLQSGKVQIAGYSKTAGNWWVIKQDDGTVAK
1570 1580 1590 1600 1610 1620

lasa_psea.pe 280 290 300 310 320 330
GQQV--SADTKLG--VYAGNINTALCEGGSSTGPHLHFSLLYNGAFVSLQGASFGPYRIN
YOMI :: : :: I I: : I::: I::: I::: I::: I::: I:::
YMHMLNTPSVKAGQSVKAGQTIGKVGSTGNSTGNHHLHLQIEQNGKTIDPE-----KYMQG
1630 1640 1650 1660 1670 1680

lasa_psea.pe 340 350 360 370
VGTSNYDNDCCRYYFYFYNQAGTTHCAFRPLYNPGLAL
YOMI :III I
IGTSISDASQAEARQQGIAQAQAKSDLLSLQGDISSVNDQIQELQYELVQSKLDEFDKRIG
1690 1700 1710 1720 1730 1740

```

FIG.-2